

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/717,789

DATE: 12/06/2000  
 TIME: 14:55:40

Input Set : A:\W078880.txt  
 Output Set : N:\CRF3\12062000\I717789.raw

**ENTERED**

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4 <110> APPLICANT: Chiorini, John
5       Kotin, Robert M.
6       Safer, Brian
8 <120> TITLE OF INVENTION: AAV5 VECTOR AND USES THEREOF
11 <130> FILE REFERENCE: 14014.0323U3
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/717,789
C--> 13 <141> CURRENT FILING DATE: 2000-11-21
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/11958
14 <151> PRIOR FILING DATE: 1999-05-28
16 <150> PRIOR APPLICATION NUMBER: 60/087,029
17 <151> PRIOR FILING DATE: 1998-05-28
19 <160> NUMBER OF SEQ ID NOS: 23
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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24 <211> LENGTH: 4652
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
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35   gcgaacgcga caagggggag agtgccacac tctcaagcaa gggggttttg taagcagtga      180
36   tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg      240
37   tgttttatcc aataggaaga aagcgcgctg atgagttctc gcgagacttc cggggtataa      300
38   aagaccgagt gaacgagccc gccgccatcc tttgctctgg actgctagag gaccctcgct      360
39   gccatggcta ccttctatga agtcattgtt cgcgtcccat ttgacgtgga ggaacatctg      420
40   cctgggaattt ctgacagctt tgtggactgg gtaactggtc aaatttggga gctgcctcca      480
41   gagtccagatt taaatttgac tctggttgaa cagcctcagt tgacggtggc tgatagaatt      540
42   cgcctcgctg tctctgacga gtggaacaaa ttttccaagc aggagtcaca attctttgtg      600
43   cagtttgaaa agggatctga atattttcat ctgcacacgc tftgtggagc ctcgggcata      660
44   tcttccatgy tctcgyccg ctaegttagt cagattcgcy cccagctggt gaaagtggtc      720
45   ttccaagga ttgaacccca gatacaacgac tgggtcgcca tcaccaaggt aaagaagggc      780
46   ggagccaata aggtggtgga ttctgggtat attccgcct acctgctgcc gaaggtccaa      840
47   ccggagcttc agtggcgctg gacaaaacctg gacgagtata aattggccgc cctgaatctg      900
48   gaggagcgca aacggctcgt cgcgcagttt ctgacagaat cctcgacgcy ctgcaggag      960
49   gcggcttcgc agcgtgagtt ctcggctgac ccggtcctca aaagcaagac ttcccaaaaa      1020
50   tacatggcgc tcgtcaactg gctcgtggag caeggcatac cttccgagaa gcagtggatc      1080
51   caggaaaatc aggagagcta cctctcttcc aactccaccy gcaactctcg gagccagatc      1140
52   aaggccgcgc tcgacaacgc gaccaaaatt atgagtctga caaaaagcgc ggtggactac      1200
53   ctctgtggga gctccgttcc cagggacatt tcaaaaaaca gaatctggca aatttttgag      1260
54   atgaatggct acgaccggc ctaegcgga tccatcctct acggctgggt tcagcgtctc      1320
55   ttcaacaaga ggaacaccgt ctggctctac ggaccgcga cgaaccggca gaccaacatc      1380
56   gcggaggcca tcgcccacac tgtgcccttt tacggctgcy tgaactggac caatgaaaac      1440
57   ttctccctta atgactgtgt ggacaaaatg ctcatttggt gggaggaggg aaagatgacc      1500
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59	aaatgtaaat	cctctgttca	aattgattct	acccctgtca	ttgtaacttc	caatacaaac	1620
60	atgtgtgttg	tgggtgatgg	gaattccacg	acctttgaac	accagcagcc	gctggaggac	1680
61	cgcattgttca	aatttgaact	gactaagcgg	ctcccgcacg	attttggcaa	gattactaag	1740
62	cagggaagtca	aggacttttt	tgcttgggca	aaggtcaatc	aggtgcccgt	gactcacgag	1800
63	tttaaaagttc	ccaggggaatt	ggcgggaact	aaagggggcg	agaaatctct	aaaacgcccc	1860
64	ctgggtgacg	tcaccaatac	tagctataaa	agctctggaga	agcgggccag	gctctcattt	1920
65	gttcccagaga	cgcctcqcag	ttcagacgtg	actgtttgat	ccgctcctct	gcgaccgctc	1980
66	aatttgaatt	caagggtatga	ttgc aaatgt	gactatcatg	ctcaatttga	caacatttct	2040
67	aacaaatgtg	atgaatgtga	atatttgaat	cggggcaaaa	atggatgtat	ctgtcacaat	2100
68	gtaactcact	gtcaaaatttg	tcattgggatt	ccccctgtgg	aaaaggaaaa	cttgtcagat	2160
69	tttggggatt	ttgacgatgc	caataaagaa	cagtaaataa	agcagtagat	catgtctttt	2220
70	gttgatcacc	ctccagattg	gttgggaagaa	gttgggtgaag	gtcttccqga	gtttttgggc	2280
71	cttgaaagcag	gcccaccgaa	accaaaccac	aatcagcagc	atcaagatca	agcccgtggt	2340
72	cttgtgtctgc	ctgggtataaa	ctatctcggg	cccggaacag	gtctcgaatg	agagagacct	2400
73	gtcaacaggg	cagacgaggt	cgcgcgagag	cagacatctc	cgtacaacga	gcagcttgag	2460
74	gcgggagaca	acccctacct	caagtacaa	cacgcggacg	ccgagtttca	ggagaagctc	2520
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76	gttctcgaac	cttttggcct	ggttgaagag	ggtgctaaga	cggccctcac	cggaaaagcgg	2640
77	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	caagccttcc	2700
78	acctcgtcag	acgcgcgaag	tggaccacag	gcatccacag	agctgcgaat	cccagcccaa	2760
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98	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	cgcgaccygc	3960
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105	gacagcaccg	gggaatcacg	aaccaccaga	cctatcggaa	cccgatacct	taccgacccc	4380
106	ctttaaccca	ttcatgtcgc	ataccctcaa	taaaccgtgt	attcgtgtca	gtaaaaatct	4440
107	gcctcttctg	gtcattccaat	gaataacagc	ttcaaacatc	tacaaaacct	ccttgccttga	4500

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108 gagtgtggca ctctccccc tgcgcgttc gctcgcgcgc tggctcggtt ggggggggtg 4560
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115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:/Note =
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123 1 5 10 15
124 Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
125 20 25 30
126 Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
127 35 40 45
128 Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
129 50 55 60
130 Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
131 65 70 75 80
132 Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
133 85 90 95
134 Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
135 100 105 110
136 Phe Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
137 115 120 125
138 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
139 130 135 140
140 Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
141 145 150 155 160
142 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
143 165 170 175
144 Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
145 180 185 190
146 Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
147 195 200 205
148 Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
149 210 215 220
150 Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
151 225 230 235 240
152 Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
153 245 250 255
154 Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
155 260 265 270
156 Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
157 275 280 285
158 Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
159 290 295 300

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160 Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
161 305 310 315 320
162 Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
163 325 330 335
164 Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
165 340 345 350
166 Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
167 355 360 365
168 Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
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174 <211> LENGTH: 610
175 <212> TYPE: PRT
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178 <220> FEATURE:
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185 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
186 20 25 30
187 Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
188 35 40 45
189 Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
190 50 55 60
191 Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
192 65 70 75 80
193 Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
194 85 90 95
195 Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
196 100 105 110
197 Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
198 115 120 125
199 Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
200 130 135 140
201 Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
202 145 150 155 160
203 Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
204 165 170 175
205 Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
206 180 185 190
207 Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
208 195 200 205
209 Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
210 210 215 220
211 Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln

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212 225          230          235          240
213 Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
214          245          250          255
215 Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
216          260          265          270
217 Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
218          275          280          285
219 Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
220          290          295          300
221 Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
222 305          310          315          320
223 Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
224          325          330          335
225 Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
226          340          345          350
227 Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
228          355          360          365
229 Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
230          370          375          380
231 Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
232 385          390          395          400
233 Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
234          405          410          415
235 Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
236          420          425          430
238 His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
239          435          440          445
240 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
241          450          455          460
242 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
243 465          470          475          480
244 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
245          485          490          495
246 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
247          500          505          510
248 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
249          515          520          525
250 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
251          530          535          540
252 Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
253 545          550          555          560
254 Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
255          565          570          575
256 Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
257          580          585          590
258 Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys
259          595          600          605
260 Glu Gln
261          610

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date